

Search

for

[Limits](#) [Preview/Index History](#) [Clipboard](#) [Details](#)

About Entrez



Text Version

Entrez PubMed

Overview

Help | FAQ

Tutorial

New/Noteworthy

E-Utilities

PubMed Services

Journals Database

MeSH Browser

Single Citation Matcher

Batch Citation Matcher

Clinical Queries

LinkOut

Cubby

Related Resources

Order Documents

NLM Gateway

TOXNET

Consumer Health

Clinical Alerts

ClinicalTrials.gov

PubMed Central

Privacy Policy

1: J Immunol 1997 Mar 15;158(6):2822-33

[Related Articles, Links](#)

Nature and origin of polymorphism in feline MHC class II DRA and DRB genes.

Yuhki N, O'Brien SJ.

Laboratory of Genomic Diversity, National Cancer Institute, Frederick Cancer Research and Development Center, MD 21702, USA.

Transcripts of the MHC class II DRA and DRB gene homologues of the domestic cat (*Felis catus*) were cloned and sequenced to compare the pattern and process of DR gene divergence. Homologous DRB exon 2 sequences from 36 feral domestic cats throughout the world plus from three species of Felidae (tiger cat, Iriomote cat, and Geoffroy's cat) were also determined. Limited variation in the domestic cat *Feca-DRA* gene was observed, but abundant variation in the *Feca-DRB* gene was seen comprising 61 distinct DRB alleles. Phylogenetic analyses resolved at least five monophyletic feline DRB allelic lineages (DRB*1 to *5), which are clearly distinct from those of human (HLA-DRB1 to 9 lineages), mouse (H-2Ebeta b, u, f), and dog DRB alleles. Approximately 80% of individual cats contained three to six distinct DRB sequences, indicating that feline MHC maintains two to three DRB loci. Five cats had three DRB sequences in a single allelic lineage, indicating the occurrence of recent gene duplication of feline DRB genes. DRB sequences isolated from three exotic cats demonstrated close association with a particular domestic cat DRB lineage, suggesting that these allelic lineages are derived from common ancestral alleles that existed prior to the divergence of these feline species about 10 to 15 million years ago. Patterns of synonymous and nonsynonymous nucleotide substitution rates that occurred in Ag recognition sites (ARS) and nonrecognition (NAR) sites demonstrated a strong role of natural selection--positive selection for Ag recognition sites and negative selection for nonrecognition sites of feline DRB sequences--in the process of evolution of DR molecules.

PMID: 9058818 [PubMed - indexed for MEDLINE]

[Write to the Help Desk](#)

[NCBI](#) | [NLM](#) | [NIH](#)

[Department of Health & Human Services](#)

[Freedom of Information Act](#) | [Disclaimer](#)

i686-pc-linux-gnu Sep 23 2002 19:02:17